

Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGATGCTGACGAGGTCAAGACATGCTTTCTCATCGGGAAGAAAGCCCCCTGTA	60
Db	1	ATGGATGCTGACGAGGTCAAGACATGCTTTCTCATCGGGAAGAAAGCCCCCTGTA	60
QY	61	AGCGATCTCCAGATGAGCGGATGAGCCATCGGCGATCCCGAGGACCTTCCACCACC	120
Db	61	AGCGATCTCCAGATGAGCGGATGAGCCATCGGCGATCCCGAGGACCTTCCACCACC	120
QY	121	TCGGGAGACAGCAAAAGCTCCAAAGAGTGACAGAGTCTGGCCAGTAATGTTAAAGTAGAG	180
Db	121	TCGGGAGACAGCAAAAGCTCCAAAGAGTGACAGAGTCTGGCCAGTAATGTTAAAGTAGAG	180
QY	181	ACTCAGAGTGATGAAGAGAAATGGCGTGCCGTGTGAATGAATGGGAGAAATGTGCGGAG	240
Db	181	ACTCAGAGTGATGAAGAGAAATGGCGTGCCGTGTGAATGAATGGGAGAAATGTGCGGAG	240
QY	241	GATTTACGAATGCTTGATGCTTCGGGAGAGAAAATGAATGGCTCCACAGGGAACCAAGCC	300
Db	241	GATTTACGAATGCTTGATGCTTCGGGAGAGAAAATGAATGGCTCCACAGGGAACCAAGCC	300
QY	301	AGCTCGGCTTTGTCGGGAGTTGAGGCATTCGACTTCCTAAGCGAAAATAAGTGTGAT	360
Db	301	AGCTCGGCTTTGTCGGGAGTTGAGGCATTCGACTTCCTAAGCGAAAATAAGTGTGAT	360
QY	361	ATCTGTGGGATCATTTTGATCGGGGCCAATGTGCTCATGGTTCACAAAAGAAAGCCACT	420
Db	361	ATCTGTGGGATCATTTTGATCGGGGCCAATGTGCTCATGGTTCACAAAAGAAAGCCACT	420
QY	421	GGAGAACGGCCCTTCAGTGCATAGTGGGGGCTCATTCACCCAGAAAGGCAACCTG	480
Db	421	GGAGAACGGCCCTTCAGTGCATAGTGGGGGCTCATTCACCCAGAAAGGCAACCTG	480
QY	481	CTCGGCACATCAAGCTGCATTCGGGGGAGAGCCCTTCAATGCCACTCTGCAACTAC	540
Db	481	CTCGGCACATCAAGCTGCATTCGGGGGAGAGCCCTTCAATGCCACTCTGCAACTAC	540
QY	541	GCCTGGCGGGAGGAGCGCCCTCACTGCCACCTGAGGAGCGCACTCGCTTGGTAAACCT	600
Db	541	GCCTGGCGGGAGGAGCGCCCTCACTGCCACCTGAGGAGCGCACTCGCTTGGTAAACCT	600
QY	601	CACAAATGTGGATATTGTGGCGAGCTATAACAGCGCAACGCTCTTTAGAGAAACATAAA	660
Db	601	CACAAATGTGGATATTGTGGCGAGCTATAACAGCGCAACGCTCTTTAGAGAAACATAAA	660
QY	661	GAGCGTGCCACAACTACTTGGAAAGCATTGGGCCCTTCGGGCACACTGTACCCAGTCATT	720
Db	661	GAGCGTGCCACAACTACTTGGAAAGCATTGGGCCCTTCGGGCACACTGTACCCAGTCATT	720
QY	721	AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGATCAGAGAGA	780
Db	721	AAAGAAGAAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGATCAGAGAGA	780
QY	781	TCCTCTGCTGGACAGACTAGCAAGTAATGTGGCCAAACGTAAGAGCTCTATGCCCTCAG	840
Db	781	TCCTCTGCTGGACAGACTAGCAAGTAATGTGGCCAAACGTAAGAGCTCTATGCCCTCAG	840
QY	841	AAATTTCTTGGGGACAAGGCGCTGTCGACACGGCCCTACGACAGTGGCCAGTACGAGAAG	900
Db	841	AAATTTCTTGGGGACAAGGCGCTGTCGACACGGCCCTACGACAGTGGCCAGTACGAGAAG	900
QY	901	GAGAAGCAAAATGATGAAGTCCCACTGTATGACCAAGCCATCAACAACGCCATCAACTAC	960
Db	901	GAGAAGCAAAATGATGAAGTCCCACTGTATGACCAAGCCATCAACAACGCCATCAACTAC	960
QY	961	CTGGGGGCGAGTCCCTGCGCCCGCTGGTGTGACAGCGCCCCGGCGGTTCCGAGGTGGTC	1020
Db	961	CTGGGGGCGAGTCCCTGCGCCCGCTGGTGTGACAGCGCCCCGGCGGTTCCGAGGTGGTC	1020
QY	1021	CCGGTTCATCAGCCCCCATGTACCAGTGCACAGGCGCTCGAGGGCAACCCCGCGCTCCAAC	1080
Db	1021	CCGGTTCATCAGCCCCCATGTACCAGTGCACAGGCGCTCGAGGGCAACCCCGCGCTCCAAC	1080

QY	1081	CACTCGGCCAGGACAGCCGGTGGAGTACCTGTGTGTCCTCTCAAGGCACAAGTTGGTG	1140
Db	1081	CACTCGGCCAGGACAGCCGGTGGAGTACCTGTGTGTCCTCTCAAGGCACAAGTTGGTG	1140
QY	1141	CCCTCGGAGCGGAGCGCTCCCGGAGCAAAGCTGCCAAGACTCCACGGACACCGAGAGC	1200
Db	1141	CCCTCGGAGCGGAGCGCTCCCGGAGCAAAGCTGCCAAGACTCCACGGACACCGAGAGC	1200
QY	1201	AACAAGGAGGAGCAGCGAGCGGTCTTATCTACCTGTAGCCAACCACATCGCCGACGCGG	1260
Db	1201	AACAAGGAGGAGCAGCGAGCGGTCTTATCTACCTGTAGCCAACCACATCGCCGACGCGG	1260
QY	1261	CAACGCGTGTGCTCAAGGAGGAGCACCGCGCCTACGACCTGCTGCGCGCGCTCCGAG	1320
Db	1261	CAACGCGTGTGCTCAAGGAGGAGCACCGCGCCTACGACCTGCTGCGCGCGCTCCGAG	1320
QY	1321	AACTCGAGGAGCGCTCCGCGTGTGAGCAACACGAGCGGGAGCAGATGAAGGTGTACAAG	1380
Db	1321	AACTCGAGGAGCGCTCCGCGTGTGAGCAACACGAGCGGGAGCAGATGAAGGTGTACAAG	1380
QY	1381	TGCGAACACTGCCGGGTGCTCTTCTGGATCAGCTCATGTACACCATCCACATGGGCTGC	1440
Db	1381	TGCGAACACTGCCGGGTGCTCTTCTGGATCAGCTCATGTACACCATCCACATGGGCTGC	1440
QY	1441	CAGCGTTCCTGTATCTTTTGTAGTCACAATGTGCGGCTTACACAGCCAGGACCGGTAC	1500
Db	1441	CAGCGTTCCTGTATCTTTTGTAGTCACAATGTGCGGCTTACACAGCCAGGACCGGTAC	1500
QY	1501	GAGTCTCTGTCGCACATAACGCGAGGGAGCACCGCTTCCACATGAGCTAA	1551
Db	1501	GAGTCTCTGTCGCACATAACGCGAGGGAGCACCGCTTCCACATGAGCTAA	1551
RESULT	2		
S80876			
LOCUS		1788 bp mRNA linear PRI 27-MAR-1997	
DEFINITION		IKAROS=hik1 {alternatively spliced} [human, Jurkat T cell line,	
ACCESSION		mRNA partial, 1788 nt].	
VERSION		S80876	
KEYWORDS		S80876.1 GI:1911482	
SOURCE		human Jurkat T cell line.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 1788)	
JOURNAL		Molnar,A., Wu,P., Largespada,D.A., Vorkamp,A., Scherer,S.,	
MEDLINE		Copeland,N.G., Jenkins,N.A., Bruns,G. and Georgopoulos,K.	
REMARK		The Ikaros gene encodes a family of lymphocyte-restricted zinc	
		finger DNA binding proteins, highly conserved in human and mouse	
		J. Immunol. 156 (2), 585-592 (1996)	
		96132984	
		GenBank staff at the National Library of Medicine created this	
		entry [NCBI gbbsq 175401] from the original journal article.	
		This sequence comes from Fig. 1B and C.	
		Map location: 7p13-p11.1.	
FEATURES		Location/Qualifiers	
source		1..1788	
		/organism="Homo sapiens"	
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		/gene="IKAROS"	
		/note="hik1"	
		238..1788	
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		/note="lymphocyte-restricted zinc finger DNA binding	
		protein: This sequence comes from Fig. 1C"	
		/codon_start=1	
		/product="hik1"	
		/protein_id="AAB50683.1"	
		/db_xref="GI:1911483"	
		/translation="MDADGODMFSFGSKESPVPVSDTPDEGPMPDPEDI-STPSSGO	

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2002, 07:06:00 ; Search time 2044.51 Seconds  
(without alignments)  
15875.226 Million cell updates/sec

Title: US-08-711-417c-165  
Perfect score: 1551  
Sequence: 1 ATGAGTCTGACGAGGTCA.....ACCGCTTCACATGAGCTAA 1551

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vt.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vt.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgtgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1551	100.0	1551	6	AR149755	AR149755 Sequence
2	1551	100.0	1788	9	S80876	S80876 IKAROS-h1k1
3	1468.8	94.7	3629	9	HSU040462	U040462 Human Ikaro
4	1386	89.4	1386	6	AR049700	AR049700 Sequence
5	1386	89.4	1386	6	AR125028	AR125028 Sequence
6	1386	89.4	1386	6	AR149594	AR149594 Sequence
7	1210	78.0	3572	9	BC018349	BC018349 Homo sapi
8	1174.8	75.7	2049	6	AR049702	AR049702 Sequence
9	1174.8	75.7	2049	6	AR125030	AR125030 Sequence
10	1174.8	75.7	2049	6	AR149596	AR149596 Sequence
11	1008	65.0	1557	5	GGKTRF	Y11833 G.gallus mR
12	888	56.0	1004	6	AR049705	AR049705 Sequence
13	868	56.0	1004	6	AR125033	AR125033 Sequence
14	868	56.0	1004	6	AR149599	AR149599 Sequence
15	814.8	52.5	1550	10	MUSIKAROS	L03547 Mouse Ikaro
16	813.2	52.4	1788	6	AR049699	AR049699 Sequence
17	813.2	52.4	1788	6	AR125027	AR125027 Sequence
18	813.2	52.4	1788	6	AR125027	AR149593 Sequence
19	754	48.6	3923	5	AF186359	AF186359 Ambystoma
20	689.4	44.4	1296	6	AR049701	AR049701 Sequence
21	689.4	44.4	1296	6	AR125029	AR125029 Sequence
22	689.4	44.4	1296	6	AR149595	AR149595 Sequence
23	682.6	44.0	2496	5	OMU92201	U92201 Oncorhynch
24	595.6	38.4	684	10	S74708	S74708 Mus muscu
25	577	37.2	1170	6	AR049703	AR049703 Sequence
26	577	37.2	1170	6	AR125031	AR125031 Sequence
27	577	37.2	1170	6	AR149597	AR149597 Sequence
28	542	34.9	1915	5	AF416370	AF416370 Danio rer
29	520.6	33.6	1287	5	AB060640	AB060640 Seriola q
30	518.2	33.4	2183	5	OMU92200	U92200 Oncorhynch
31	499	32.2	2309	5	AF092175	AF092175 Danio rer
32	496.8	32.0	2375	5	AF163848	AF163848 Raja egla
33	479.2	30.9	203352	2	AL596450	AL596450 Mus muscu
34	460.2	29.7	2301	5	OMU92198	U92198 Oncorhynch
35	458.2	29.5	1128	6	AR049704	AR049704 Sequence
36	458.2	29.5	1128	6	AR125032	AR125032 Sequence
37	458.2	29.5	1128	6	AR149598	AR149598 Sequence
38	420.2	27.1	1485	5	GGA005933	AJ005933 Gallus ga
39	414.6	26.7	2098	5	AF129512	AF129512 Homo sapi
40	412.4	26.6	1672	5	AF163850	AF163850 Raja egla
41	411.8	26.6	1521	10	AF001293	AF001293 Mus muscu
42	409.2	26.4	1876	5	AF163847	AF163847 Raja egla
43	408	26.3	2490	9	AF130863	AF130863 Homo sapi
44	404.8	26.1	1847	10	AF044257	AF044257 Mus muscu
45	394	25.4	1639	5	AF416371	AF416371 Danio rer

ALIGNMENTS

RESULT 1	AR149755	AR149755	Sequence	1551 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR149755	Sequence	165 from patent US 6228611.				
DEFINITION	AR149755	Sequence	165 from patent US 6228611.				
ACCESSION	AR149755	Sequence	165 from patent US 6228611.				
VERSION	AR149755.1	GI:15114346					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1551)						
AUTHORS	Georgopoulos,K.						
TITLE	Ikaro: A T cell pathway regulatory gene						
JOURNAL	Patent: US 6228611-A 165 08-MAY-2001;						
FEATURES	Location/Qualifiers						
source	1..1551						
BASE COUNT	393 a	450 c	443 g	265 t			
ORIGIN							

Query Match 100.0%; Score 1551; DB 6; Length 1551;  
Best Local Similarity 100.0%; Pred. No. 2.5e-250;

OSKSDRVASNVKVTQSDENGACEMNGEBCEADLRMLDASGEKMGSHRDGSS  
 ALSVGGRLPFGKLCIDIGIICGNVLMVHRSHITGERPQCNOCCASFTOKGNL  
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 HKERCHNYLESMLPGTLYPVKEETKHSEMDLCKIGISERSLVLDRLASVAKRKS  
 SMPQKFLGDKLSLTPYDSATYKEENEMKSHVMDQAINNAINYLGAESLRPLVQTPP  
 GSEVVPVSPMYOLHRRSRGTPSRNHSQAQDSAVEYLLLSLAKLVPSREASPNSC  
 QDSTDTSNNEORSGLIYLTNIIARRAQRVSLKEEHRAYDLRLAASNSDALRVYS  
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 GEHRFHS"

BASE COUNT 450 a 511 c 497 g 330 t  
 ORIGIN

Query Match 100.0%; Score 1551; DB 9; Length 1788;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-250;  
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATGCTGACGAGGGTCAAGACATCTCTTCTCATCAGGGAAGAAAGCCCCCTGTGA 60  
 DB 238 ATGGATGCTGACGAGGGTCAAGACATCTCTTCTCATCAGGGAAGAAAGCCCCCTGTGA 297  
 QY 61 AGCGATATCTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACACC 120  
 DB 298 AGCGATATCTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACACC 357  
 QY 121 TCGGAGGACAGCAAGCTCCAGAGTGCAGAGTCTGTGGCCAGTAATGTTAAAGTAGAG 180  
 DB 358 TCGGAGGACAGCAAGCTCCAGAGTGCAGAGTCTGTGGCCAGTAATGTTAAAGTAGAG 417  
 QY 181 ACTCAGATGATGAGAGATGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGCGGAG 240  
 DB 418 ACTCAGATGATGAGAGATGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGCGGAG 477  
 QY 241 GATTACGAATGCTTGATGCTCGGAGAGAAATGAATGGTCCCAAGGACCAAGGC 300  
 DB 478 GATTACGAATGCTTGATGCTCGGAGAGAAATGAATGGTCCCAAGGACCAAGGC 537  
 QY 301 AGCTCGGCTTTGTCGGAGTGTGAGGATTCGACTTCCTTAACGGAATAAAGTGTGAT 360  
 DB 538 AGCTCGGCTTTGTCGGAGTGTGAGGATTCGACTTCCTTAACGGAATAAAGTGTGAT 597  
 QY 361 ATCTGTGGGATCATTTGCACTCGGGCCCAATGTCTCATGTTTCATGAGGACCACT 420  
 DB 598 ATCTGTGGGATCATTTGCACTCGGGCCCAATGTCTCATGTTTCATGAGGACCACT 657  
 QY 421 GGAGACGGCCCTTCAGTGTCAATAGTCCGGGGCTCATTCACCCAGGAAGGCAACCTG 480  
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 QY 541 GCTCTCGCGGAGGACGCCCTCACTGCGCCACCTGAGGAGCGCACTCCGTTGGTAAACCT 600  
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 QY 601 CACAAATGTGATATGTGGCCGAGCTATAAAGAGGAAAGCTTTAGAGGAACATAAA 660  
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 QY 721 AAAGAGAAACTAAGACAGTGAATGGCAGAGACCTGTGAGATAGGATCAGAGAGA 780  
 DB 958 AAAGAGAAACTAAGACAGTGAATGGCAGAGACCTGTGAGATAGGATCAGAGAGA 1017  
 QY 781 TCTCTCGTGTGACAGACTAGCAAGTAATGCCCAAACGTAAGAGCTCTATSCCTCAG 840  
 DB 1018 TCTCTCGTGTGACAGACTAGCAAGTAATGCCCAAACGTAAGAGCTCTATSCCTCAG 1077

QY 841 AAATTTCTTGGGGAACAAGGGCTGTCCGACACGGCCCTACGACAGTGCACGCTACGAGAAG 900  
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 DB 1318 CACTCGGCCCAGGACAGCGCGCTGGAGTACTGCTGCTCTCTCCAAAGGCCAAGTTGGTG 1377  
 QY 1141 CCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGC 1200  
 DB 1378 CCCTCGGAGCGGAGGCGTCCCGGAGCAACAGCTGCCAAGACTCCACGACACCGAGAGC 1437  
 QY 1201 AACAAAGGAGGACAGCGCGCTTATCTACTGACCAACACATCGCCGACGCGCG 1260  
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 QY 1501 GAGTCTCTGTCGACATACGCGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1551  
 DB 1738 GAGTCTCTGTCACATACACGCGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1788

## RESULT 3

HSU40462

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

HSU40462 3629 bp mRNA linear PRI 27-APR-1996  
 Human Ikaros/LyF-1 homolog (hIk-1) mRNA, complete cds.

U40462.1 GI:1289370

human.  
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3629)  
 Niefeld, W. and Meyerhans, A.

Cloning and sequencing of hIk-1, a cDNA encoding a human homologue  
 of mouse Ikaros/LyF-1

Immunol. Lett. 49 (1-2), 139-141 (1996)

96252222  
 2 (bases 1 to 3629)  
 Niefeld, W.

Direct Submission

Submitted (10-NOV-1995) Wilfried Niefeld, Department of Virology,  
 University of Freiburg, Institute for Medical Microbiology and

Hygiene, Hermann-Herder-Strasse 11, Freiburg 79104, Germany

Location/Qualifiers

source 1. 3629 /organism="Homo sapiens" /db\_xref="taxon:9606" /tissue\_type="bone marrow" 1. 3629 /gene="hik-1" 169. 1728 /gene="hik-1" /note="similar to mouse Lyf-1, encoded by GenBank Accession Number S74708; similar to mouse Ikaros DNA-binding protein, Swiss-Prot Accession Number Q03267" /codon\_start=1 /product="Ikaros/Lyf-1 homolog" /protein\_id="AAC50459.1" /db\_xref="GI:1289371" /translation="MDADGQMSQVSKESPVSYPDDEDEMPEDLSTTSQGO QSSKSDRVASNVKVEQSDENGRACEMNGEACEADLRMLDASGERKMSHRDQSS ALSGVGTRLENGKLDICIGIPNLMVHKRSHTRPFQNCQSGASFTQKGNL LRHLKSGEPFFKCHLCNACRRDALTGHLRTHSVGPKGCGYGRSFKORSLPE HKERCHNLYESLPGDILYPIKKEETHNHEMAEDLCKIGSERSLVLRASNAKRKS SMPQKFLDGKLSLTPYDSSASKEKEMMSKSHVNDQAINNAIYLGAEISRLVOTP PGSSVDPVISPMTQLHKPLAEGTPRSNHSQDSAVENLLLSLRAKLVPPSERASPSN SCODSTDPESEMQRSGLIYLTNIAPHARNGLSLKEHRAVLDLLRAAENSODALR VYSNLSGEOMKVVYKEHCRVFLDHWMTIHMGCCHGFRDPFECNMCGYHSODRYEFSSH ITRGHRPHMS"

BASE COUNT 917 a 1002 c 936 g 773 t 1 others

Query Match 94.7%; Score 1468.8; DB 9; Length 3629; Best Local Similarity 97.7%; Pred. No. 1.3e-236; Matches 1524; Conservative 0; Mismatches 27; Indels 9; Gaps 3;

QY 1 ATGGATCTGACGAGGCTCAAGACATGCTTTCTCATCAGGAGGAAGACCCCTGTA 60  
DB 169 ATGGATCTGATGAGGCTCAAGACATGCTCCCAAGTTTTCAGGAGGAAGACCCCTGTA 228  
QY 61 AGCGATCTCCAGTGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACACC 120  
DB 229 AGCGATCTCCAGTGGGCGATGAGCCCATGCCGATCCCGAGGACCTCTCCACACC 288  
QY 121 TCGGAGGACAGCAAGCTCCAGAGTGACAGAGTCTGGGCGAGTAATGTTAAAGTAGAG 180  
DB 289 TCGGAGGACAGCAAGCTCCAGAGTGACAGAGTCTGGGCGAGTAATGTTAAAGTAGAG 348  
QY 181 ACTCAGAGTATGAGAGATGGCGCTGTGAATGATGGGAGAAATGTCGGGAG 240  
DB 349 ACTCAGAGTATGAGAGATGGCGCTGTGAATGATGGGAGAAATGTCGGGAG 408  
QY 241 GATTTAGCAATGCTTGATGCTCGGAGAGAAATGATGGCTCCACAGGGGACCAAGGC 300  
DB 409 GATTTAGCAATGCTTGATGCTCGGAGAGAAATGATGGCTCCACAGGGGACCAAGGC 468  
QY 301 AGCTCGGCTTTGTCGGAGTTGGAGGCAATTCGACTTCTTAACGAGAAACTAAAGTGTAT 360  
DB 469 AGCTCGGCTTTGTCGGAGTTGGAGGCAATTCGACTTCTTAACGAGAAACTAAAGTGTAT 528  
QY 361 ATCTGTGGGATCATTTGATCGGCGCCCAATGTGCTCATGTGTTACAAAAGAACCCACACT 420  
DB 529 ATCTGTGGGATCATTTGATCGGCGCCCAATGTGCTCATGTGTTACAAAAGAACCCACACT 588  
QY 421 GGAGAACGGCCCTCCAGTCAATAGTGGGGCCCTCATTCACCCAGAGAGGCAACCTG 480  
DB 589 GGAGAACGGCCCTCCAGTCAATAGTGGGGCCCTCATTCACCCAGAGAGGCAACCTG 648  
QY 481 CTCGGGACATCAAGCTCATTCGGGGAGAGGCGCTTCAATGCCACCTCTGCAACTAC 540  
DB 649 CTCGGGACATCAAGCTCATTCGGGGAGAGGCGCTTCAATGCCACCTCTGCAACTAC 708  
QY 541 GCCTCGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCGGTGGTAAACCT 600  
DB 709 GCCTCGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCGGTGGTAAACCT 768

QY 601 CACAATGTGGATATTGTGGCCGAAGCTATATAACAGCGAAGCTCTTTAGAGAAACATAA 660  
DB 769 CACAATGTGGATATTGTGGCCGAAGCTATATAACAGCGAAGCTCTTTAGAGAAACATAA 828  
QY 661 GAGCGTGCACCAACTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCCACTCAT 720  
DB 829 GAGCGTGCACCAACTACTTGGAAAGCATGGGCTTCCGGGCACACTGTACCCACTCAT 888  
QY 721 AAAGAAGAAGCACTAAGCAGAGTGAATGGCAGAGAGCTGTGCAAGATAGGATCAGAGAGA 780  
DB 889 AAAGAAGAAGCACTAAGCAGAGTGAATGGCAGAGAGCTGTGCAAGATAGGATCAGAGAGA 948  
QY 781 TCTCTCGTGTGACAGACTAGCAAGTAATGTGCGCAAAAGCTAAGAGCTCTATGCTCTAG 840  
DB 949 TCTCTCGTGTGACAGACTAGCAAGTAATGTGCGCAAAAGCTAAGAGCTCTATGCTCTAG 1008  
QY 841 AAATTTCTTGGGACAGAGGCTGTCCGACACGCCCTACGAG ---CAGTGCCACGTACGAG 897  
DB 1009 AAATTTCTTGGGACAGAGGCTGTCCGACACGCCCTACGAG ---CAGTGCCACGTACGAG 1068  
QY 898 AAGGAGAAACGAATGATGAAGTCCACGTGATGGACCAAGCCATCAACAGCCCATCAAC 957  
DB 1069 AAGGAGAAACGAATGATGAAGTCCACGTGATGGACCAAGCCATCAACAGCCCATCAAC 1128  
QY 958 TACCTGGGGCGGAGTCCCTGCGCGCGCTGTCAGAGCGCCCGCGGCTTCCGAGGTTG 1017  
DB 1129 TACCTGGGGCGGAGTCCCTGCGCGCGCTGTCAGAGCGCCCGCGGCTTCCGAGGTTG 1188  
QY 1018 GTCCCGTCTATCAGCCCGATGTACAGCTGCACA ---GGCGCTCGGAGGACACCCCGCGC 1074  
DB 1189 GTCCCGTCTATCAGCCCGATGTACAGCTGCACAAGCGCTCGCGGAGGACACCCCGCGC 1248  
QY 1075 TCCAACCACTCGGCGCGAGGACAGCGCGCTGTCAGAGTCTGCTCTCCAGAGGCAAG 1134  
DB 1249 TCCAACCACTCGGCGCGAGGACAGCGCGCTGTCAGAGTCTGCTCTCCAGAGGCAAG 1308  
QY 1135 TTGCTGCTCGGAGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC 1194  
DB 1309 TTGCTGCTCGGAGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGGACACC 1368  
QY 1195 GAGAGCAACACGAGGAGGACAGCGCGCTTATCTACCTGACCAACCACTCGCCCGG 1254  
DB 1369 GAGAGCAACACGAGGAGGACAGCGCGCTTATCTACCTGACCAACCACTCGCCCGG 1428  
QY 1255 GCGCGC ---AACGCTGCTCCTCAAGGAGGAGCAGCGCGCTACGACCTGCTCGCGGC 1311  
DB 1429 CAGCGCGCAACGCGCTTCTCCTCAAGGAGGAGCAGCGCGCTACGACCTGCTCGCGGC 1488  
QY 1312 GCCTCCGAGAACTCGCAGGACGCGCTCCGCTGTGTGTCAGCAGCGGGGACGATGAAG 1371  
DB 1489 GCCTCCGAGAACTCGCAGGACGCGCTCCGCTGTGTGTCAGCAGCGGGGACGATGAAG 1548  
QY 1372 GTGTACAAGTGGGAACACTGCGGGGTGCTTCTCTGGATACAGTATACCATCCAC 1431  
DB 1549 GTGTACAAGTGGGAACACTGCGGGGTGCTTCTCTGGATACAGTATACCATCCAC 1608  
QY 1432 ATGGCTGCGCAGCGCTTCCGCTGATCCTTTGAGTGCAACATGTGGGTACACAGCCAG 1491  
DB 1609 ATGGCTGCGCAGCGCTTCCGCTGATCCTTTGAGTGCAACATGTGGGTACACAGCCAG 1668  
QY 1492 GACCGGTAGAGTTCTGTCGCACATACGCGGAGGAGCAGCGCTTCCACATAGCTAA 1551  
DB 1669 GACCGGTAGAGTTCTGTCGCACATACGCGGAGGAGCAGCGCTTCCACATAGCTAA 1728

RESULT 4  
AR049700  
LOCUS AR049700 1386 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 3 from patent US 5824770.  
ACCESSION AR049700  
VERSION AR049700.1 GI:5971692  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1386)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros polypeptides  
JOURNAL Patent: US 5824770-A 3 20-Oct-1998;  
FEATURES Location/Qualifiers  
1..1386  
source /organism="unknown"  
BASE COUNT 350 a 403 c 395 g 238 t  
ORIGIN

Query Match 89.4%; Score 1386; DB 6; Length 1386;  
Best Local Similarity 100.0%; Pred. No. 1.le-222;  
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAATGAATGGG 225  
Db 1 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAATGAATGGG 60

QY 226 GAAGAATGTGCGGAGGATTTACGATGATGCTTCGGGAGAGAAATGAATGGCTCC 285  
Db 61 GAAGATGTGCGGAGGATTTACGATGATGCTTCGGGAGAGAAATGAATGGCTCC 120

QY 286 CACAGGACCAAGGACGCTCGGCTTTGTCGGGAGTTGGAGGATTCGACTTCCTAACGGA 345  
Db 121 CACAGGACCAAGGACGCTCGGCTTTGTCGGGAGTTGGAGGATTCGACTTCCTAACGGA 180

QY 346 AAACATAAGTGTGATATCTGTGGGATCATTTGCATCGGSCCAATGTGCTCATGTTTAC 405  
Db 181 AAACATAAGTGTGATATCTGTGGGATCATTTGCATCGGSCCAATGTGCTCATGTTTAC 240

QY 406 AAAAGAGGCACACTGGAGAACGSCCTTCCAGTGAATCACTGGGGGCGCTTATTACCC 465  
Db 241 AAAAGAGGCACACTGGAGAACGSCCTTCCAGTGAATCACTGGGGGCGCTTATTACCC 300

QY 466 CAGAGGGCAACCTGCTCCGGACATCAAGCTGCAATTCGGGGAGAGCCCTTCAAAATGC 525  
Db 301 CAGAGGGCAACCTGCTCCGGACATCAAGCTGCAATTCGGGGAGAGCCCTTCAAAATGC 360

QY 526 CACTCTGCAACTACCGCTCCCGCGGAGGAGCGCTCACTGGCCCACTGAGGACGCAC 585  
Db 361 CACTCTGCAACTACCGCTCCCGCGGAGGAGCGCTCACTGGCCCACTGAGGACGCAC 420

QY 586 TCGGTTGGTAAACCTCACAATGTGGATATTGTGCGGAGGATTAACACGCGACGCTCT 645  
Db 421 TCGGTTGGTAAACCTCACAATGTGGATATTGTGCGGAGGATTAACACGCGACGCTCT 480

QY 646 TTAGAGGAACATAAGAGCGCTGCCACAACTACTTTGAAAGCATGGGCTTTCCGGGCACA 705  
Db 481 TTAGAGGAACATAAGAGCGCTGCCACAACTACTTTGAAAGCATGGGCTTTCCGGGCACA 540

QY 706 CTGTACCCAGTCATTAAAGAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 765  
Db 541 CTGTACCCAGTCATTAAAGAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAG 600

QY 766 ATAGATCAGAGATCTCTGCTGTGCAGACACTAGCAAGTAATGTGCGCAACAGTAAG 825  
Db 601 ATAGATCAGAGATCTCTGCTGTGCAGACACTAGCAAGTAATGTGCGCAACAGTAAG 660

QY 826 AGCTCTATGCTCAGAAATTTCTGGGAGCAAGGGCTTGTCCGACAGCGCTTACGACAGT 885  
Db 661 AGCTCTATGCTCAGAAATTTCTGGGAGCAAGGGCTTGTCCGACAGCGCTTACGACAGT 720

QY 886 GCCAGTACGAGAGGAGAGCAATGATGAAGTCCACGCTGATGGACCAAGCCATCAAC 945  
Db 721 GCCAGTACGAGAGGAGAGCAATGATGAAGTCCACGCTGATGGACCAAGCCATCAAC 780

QY 946 AACGCCATCACTACCTGGGGGCGAGTCCCTGGGCCGCTGTGTGAGAGCGCCCGGGC 1005  
Db 781 AACGCCATCACTACCTGGGGGCGAGTCCCTGGGCCGCTGTGTGAGAGCGCCCGGGC 840

QY 1006 GGTTCGAGGTGGTCCCGGTTCATCAGCCCGGATGATACAGCGCTCGGAGGC 1065  
Db 841 GGTTCGAGGTGGTCCCGGTTCATCAGCCCGGATGATACAGCGCTCGGAGGC 900

QY 1066 ACCCGCGCTCCAAACCACTCGCGCCAGGACAGCGCTGAGTACCTGCTGCTCTCC 1125  
Db 901 ACCCGCGCTCCAAACCACTCGCGCCAGGACAGCGCTGAGTACCTGCTGCTCTCC 960

QY 1126 AAGGCCAAGTTGGTGGCTCGGAGCGGAGCGGTCCCGAGCAACAGCTGCCAAGACTCC 1185  
Db 961 AAGGCCAAGTTGGTGGCTCGGAGCGGAGCGGTCCCGAGCAACAGCTGCCAAGACTCC 1020

QY 1186 ACGGACCCGAGAGCAACAAGAGGAGCAGCGAGCGGTCTTATCTACCTGACCAACCAC 1245  
Db 1021 ACGGACCCGAGAGCAACAAGAGGAGCAGCGAGCGGTCTTATCTACCTGACCAACCAC 1080

QY 1246 ATCCCGCGAGCGCGCAACCGCTGTGCTCAAGGAGGAGCACCAGCGCTTACGACCTGCTG 1305  
Db 1081 ATCCCGCGAGCGCGCAACCGCTGTGCTCAAGGAGGAGCACCAGCGCTTACGACCTGCTG 1140

QY 1306 CGCGCCGCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTCAGCACCAGCGGAGCAG 1365  
Db 1141 CGCGCCGCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTCAGCACCAGCGGAGCAG 1200

QY 1366 ATGAAGGTGTACAGTCCGAACTCGCGGGTGTCTTCTCGATCAGCTCATGTATACACC 1425  
Db 1201 ATGAAGGTGTACAGTCCGAACTCGCGGGTGTCTTCTCGATCAGCTCATGTATACACC 1260

QY 1426 ATCCACATGGCTGCCACGGCTTCCGTGATCCTTTTGTAGTGAACATGTGCGGCTTACCAC 1485  
Db 1261 ATCCACATGGCTGCCACGGCTTCCGTGATCCTTTTGTAGTGAACATGTGCGGCTTACCAC 1320

QY 1486 AGCAGGACCGGTACGAGTTCCTGCGCACATAACGCGGAGGAGCAGCGCTTCCACATG 1545  
Db 1321 AGCAGGACCGGTACGAGTTCCTGCGCACATAACGCGGAGGAGCAGCGCTTCCACATG 1380

QY 1546 AGCTAA 1551  
Db 1381 AGCTAA 1386

RESULT 5  
LOCUS AR125028 1386 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 2 from patent US 6172278.  
ACCESSION AR125028  
VERSION AR125028.1 GI:14110412  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1386)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros transgenic cells and mice  
JOURNAL Patent: US 6172278-A 2 09-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..1386  
BASE COUNT 350 a 403 c 395 g 238 t  
ORIGIN

Query Match 89.4%; Score 1386; DB 6; Length 1386;  
Best Local Similarity 100.0%; Pred. No. 1.le-222;  
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAATGAATGGG 225  
Db 1 AATGTTAAAGTAGAGACTCAGAGTGAAGAGAAATGGCGTGCCTGTGAATGAATGGG 60

QY 226 GAAGAATGTGCGGAGGATTTACGATGATGCTTCGGGAGAGAAATGAATGGCTCC 285  
Db 61 GAAGAATGTGCGGAGGATTTACGATGATGCTTCGGGAGAGAAATGAATGGCTCC 120

1366 ATGAAGTCTCAAGTGGCAACACTGCCGGTGTCTTCTCTGGATCAGCTCATGTACACC 1425  
1201 ATGAAGTGTACAAGTGGCAACACTGCCGGTGTCTTCTCTGGATCAGCTCATGTACACC 1260  
1426 ATCCACATGGCTGCCACCGCTTCCGTGATCTTTTGTAGTGAACATGTGCGCTTACCAC 1485  
1261 ATCCACATGGCTGCCACCGCTTCCGTGATCTTTTGTAGTGAACATGTGCGCTTACCAC 1320  
1486 AGCCAGGACCGGTACGAGTCTCTGTCGCACATAACCGAGGAGGACACCGCTTCCACATG 1545  
1321 AGCCAGGACCGGTACGAGTCTCTGTCGCACATAACCGAGGAGGACACCGCTTCCACATG 1380  
1546 AGCTAA 1551  
1381 AGCTAA 1386

RESULT 6  
LOCUS AR149594 1386 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 3 from patent US 6228611.  
ACCESSION AR149594  
VERSION AR149594.1 GI:15114185  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1386)  
AUTHORS Georgopoulos, K.  
TITLE Ikaros: A T cell pathway regulatory gene  
JOURNAL Patent: US 6228611-A 3 08-MAY-2001;  
FEATURES Location/Qualifiers  
source .1.1386  
BASE COUNT 350 a 403 c 395 g 238 t  
ORIGIN

286 CACAGGGACCAAGCAGCTCGGCTTTGTGGAGTTGGAGGCAATTCGACTTCCTTAACGGA 345  
121 CACAGGGACCAAGCAGCTCGGCTTTGTGGAGTTGGAGGCAATTCGACTTCCTTAACGGA 180  
346 AAACATAAGTGTGATATCTGTGGATCATTTTGCATCGGGCCCAATGTGCTCATGTTTAC 405  
181 AAACATAAGTGTGATATCTGTGGATCATTTTGCATCGGGCCCAATGTGCTCATGTTTAC 240  
406 AAAGAAGCCACACTGGAGACGGCCCTTCCAGTGCATATGTCGGGGCCCTCATTCACC 465  
241 AAAGAAGCCACACTGGAGACGGCCCTTCCAGTGCATATGTCGGGGCCCTCATTCACC 300  
466 CAGAAGGGCAACTCTGTCGGGCACATCAAGTGCATTTCCGGGGAAGACCCCTTCAATGC 525  
301 CAGAAGGGCAACTCTGTCGGGCACATCAAGTGCATTTCCGGGGAAGACCCCTTCAATGC 360  
526 CACCTCTGCAACTAGCCCTGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGAC 585  
361 CACCTCTGCAACTAGCCCTGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGAC 420  
586 TCGGTTGGTAAACCTCACAATGTGGATATTTGTGGCCGAAGCTATAAAGCGAAGCTGT 645  
421 TCGGTTGGTAAACCTCACAATGTGGATATTTGTGGCCGAAGCTATAAAGCGAAGCTGT 480  
646 TTAGAGAAACATAAAGAGCGCTGCCACACTACTTGGAAAGCATGGCTTCCGGGCACA 705  
481 TTAGAGAAACATAAAGAGCGCTGCCACACTACTTGGAAAGCATGGCTTCCGGGCACA 540  
706 CTGTACCCAGTCAATTAAGAAGAACTAAAGCAGTGAATGGCAGAACCTGTGCAAG 765  
541 CTGTACCCAGTCAATTAAGAAGAACTAAAGCAGTGAATGGCAGAACCTGTGCAAG 600  
766 ATAGGATCAGAGAGATCTCTGCTGTGGACAGACTAGCAAGTAATGTCGCCAAAGCTAAG 825  
601 ATAGGATCAGAGAGATCTCTGCTGTGGACAGACTAGCAAGTAATGTCGCCAAAGCTAAG 560  
826 AGCTCTATGCTCAGAAATTTCTTGGGACAAAGGCGCTGTCCGACACGCGCTACGACAGT 885  
661 AGCTCTATGCTCAGAAATTTCTTGGGACAAAGGCGCTGTCCGACACGCGCTACGACAGT 720  
886 GCCACGTACGAGAGAGAGAAATGATGAATGCTCCAGTGTGACCAAGCCATCAAC 945  
721 GCCACGTACGAGAGAGAGAAATGATGAATGCTCCAGTGTGACCAAGCCATCAAC 780  
946 AACGCCATCAACTACCTGGGGGCGGAGTCCCTGCGCCGCTGTGTCAGACGCGCCCGGGC 1005  
781 AACGCCATCAACTACCTGGGGGCGGAGTCCCTGCGCCGCTGTGTCAGACGCGCCCGGGC 840  
1006 GTTTCGAGGTGGTCCCGGTCATCAGCCCGATGTACAGCTGTGACAGGCGCTCGGAGGGC 1065  
841 GTTTCGAGGTGGTCCCGGTCATCAGCCCGATGTACAGCTGTGACAGGCGCTCGGAGGGC 900  
1066 ACCCGCGCTCCACCACTCGGCGCCAGGACAGCGCGCTGGAGTACCTGCTGCTCTCC 1125  
901 ACCCGCGCTCCACCACTCGGCGCCAGGACAGCGCGCTGGAGTACCTGCTGCTCTCC 960  
1126 RAGGCAAGTGGTGGCTCTCGAGCGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCC 1185  
961 RAGGCAAGTGGTGGCTCTCGAGCGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCC 1020  
1186 AGGACACCGAGAGCAACAGAGAGAGCGGCGATCTTATCTACCTGACCAACAC 1245  
1021 AGGACACCGAGAGCAACAGAGAGAGCGGCGATCTTATCTACCTGACCAACAC 1080  
1246 ATGCGCCGACGCGGCAAGCGTGTCTCAAGGAGGAGCAGCGCTTACGACTGCTG 1305  
1081 ATGCGCCGACGCGGCAAGCGTGTCTCAAGGAGGAGCAGCGCTTACGACTGCTG 1140  
1306 CGCGCGCTCCGAGAACTCGCAGGACGCGCTTCCGCTGGTTCAGACACGCGGGAGCAG 1365  
1141 CGCGCGCTCCGAGAACTCGCAGGACGCGCTTCCGCTGGTTCAGCAGCAGCGGGAGCAG 1200

Query Match 89.4%; Score 1386; DB 6; Length 1386;  
Best Local Similarity 100.0%; Pred. No. 1.1e-222;  
Matches 1386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;











RESULT	10
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ARL149596	ARL149596	2049 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	Sequence 5 from patent US 6228611.				
DEFINITION	Sequence 5 from patent US 6228611.				
ACCESSION	ARL149596				
VERSION	ARL149596.1	GI:15114187			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2049)				
AUTHORS	Georgopoulos,K.				
TITLE	Ikaros: A T cell pathway regulatory gene				
JOURNAL	Patent: US 6228611-A 5 08-MAY-2001;				
FEATURES	Location/Qualifiers				
source	1..2049				
BASE COUNT	514 a 531 c 574 g 430 t				
ORIGIN					
	Query Match	75.7%;	Score 1174.8;	DB 6;	Length 2049;
	Best Local Similarity	87.2%;	Pred. No. 2.4e-187;	Indels	24;
	Matches 1365;	Conservative	0;	Mismatches 177;	Gaps
QY	1	ATGGATGCTGACGAGGGTCAAGACATGCTTTCTTCATCAGGAAGAAAGCCCCCTGTA	60		
DB	223	ATGGATGTCGATGAGGGTCAAGACATGTCACCAAGTTTCAGAAAGAGAGCCCCCAGTC	282		
QY	61	AGCGATATCCAGATGAGGGGATGAGCCCATGCGGATCCCGAGAGACTCTCCACACC	120		
QY	283	AGTGACATCCAGATGAGGGGATGAGCCCATGCTGTCCTGAGGACCTGTCCACTACC	342		
DB	283	AGTGACATCCAGATGAGGGGATGAGCCCATGCTGTCCTGAGGACCTGTCCACTACC	342		
QY	121	TCGGGAGGACAGCAAGCTCCAAAGAGTACAGAGTCTGTGCGCAGTAAATGTTAAAGTAGAG	180		
DB	343	TCGGGAGGACAGCAAGCTCCAAAGAGTATCGAGGATGCGCAGTAAATGTTAAAGTAGAG	402		
QY	181	ACTCAGAGTGATGAAGAAATGGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGGCGGAG	240		
DB	403	ACTCAGAGTGATGAAGAAATGGGCGTGCCTGTGAATGAATGGGGAAGAAATGTGGCGGAG	462		
QY	241	GATTTACGAATGCTTGATGCTCGGAGAGAAAATGAATGCTCCACAGGGACCAAGGC	300		
DB	463	GATTTACGAATGCTTGATGCTCGGAGAGAAAATGAATGCTCCACAGGGACCAAGGC	522		
QY	301	AGCTCGGCTTTGTCGGGAGTTGGAGCATTCGACATTCCTAACGGAAAACATAAGTGTGAT	360		
DB	523	AGCTCGGCTTTGTCGGGAGTTGGAGCATTCGACATTCCTAACGGAAAACATAAGTGTGAT	582		
QY	361	ATCTGTGGATCATTTTCATCGGGGCCAATGTGCTATGCTGTTTCACAAAGAGCCACACT	420		
DB	583	ATCTGTGGATCATTTTCATCGGGGCCAATGTGCTATGCTGTTTCACAAAGAGCCACACT	642		
QY	421	GGAGAACGGCCCTTCAGATGCAATCAGTTCGGGGCCCTCATTCACCCAGAAAGGCAACCTG	480		
DB	643	GGTGAACGGCCCTTCACAGTGCACCACTGTGGGGCTCCCTTTACCCAGAAAGGCAACCTC	702		
QY	481	CTCCGGCACATCAAGCTGCATTCGGGGGAGAGCCCTTCAATGTCACCTCTGCAACTAC	540		
DB	703	CTCCGGCACATCAAGCTGCATTCGGGGGAGAGCCCTTCAATGTCACCTCTGCAACTAT	762		
QY	541	GCTTCGCGCGGAGGGAGCCCTCAGTGGCCACTGAGGACGACCTCCGTTGGTAAAGCT	600		
DB	763	GCTTCGCGCGGAGGGAGCCCTCAGTGGCCACTGAGGACGACCTCCGTTGGTAAAGCT	822		
QY	601	CACAAATGTGGATATGTGGCCGAGCTATTAACAGGACGCTCTTTAGAGGAACATAAA	660		
DB	823	CACAAATGTGGATATGTGGCCGAGCTATTAACAGGACGCTCTTTAGAGGAACATAAA	882		
QY	661	GAGCGTGCACAACTACTTGGAAAGCATGGCCCTTCGGGGCACACTGTACCCAGTCATT	720		
DB	883	GAGCGTGCACAACTACTTGGAAAGCATGGCCCTTCGGGGCACACTGTACCCAGTCATT	939		
QY	721	AAAGAAAGAACTAAGCACAGTGAATGCCAGAGACCTGTGCAAGATAGGATCAGAGAGA	780		



QY 1492 GACCGTACGAGTCTCTGTCGCACATAACGCGAGGGAGCACCGCTTCCACATGAGCTAA 1551  
DB 1498 GACAGGTGAATTTTCTTCCACATAACTCGAGGGAGCACCGTTTCCACATGAGTTAA 1557

RESULT 12  
AR049705 AR049705 1004 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 8 from patent US 5824770.  
DEFINITION AR049705  
ACCESSION AR049705  
VERSION AR049705.1 GI:5971697  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1004)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros polypeptides  
JOURNAL Patent: US 5824770-A 8 20-OCT-1998;  
FEATURES Location/Qualifiers  
source 1..1004  
BASE COUNT 235 a 328 c 286 g 155 t  
ORIGIN

Query Match 56.0%; Score 868; DB 6; Length 1004;  
Best Local Similarity 88.8%; Pred. No. 6.2e-136;  
Matches 1004; Conservative 0; Mismatches 0; Indels 126; Gaps 1;

QY 421 GGAGAACGGCCCTTCCAGTGCATTCAGTGGCGGCTCATTCACCCAGAGGGCAACCTG 480  
DB 421 GGAGAACGGCCCTTCCAGTGCATTCAGTGGCGGCTCATTCACCCAGAGGGCAACCTG 60

QY 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 540  
DB 61 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 120

QY 541 GCCTGCCCGCGAGGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600  
DB 121 GCCTGCCCGCGAGGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCC----- 168

QY 601 CACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGAGCTCTTTAGAGGAACATAAA 660  
DB 169 ----- 168

QY 661 GAGCGCTGCCACACTACTTGGAAAGCATGGGCTTCCGGGACACACTGTACCCAGTCAAT 720  
DB 169 -----GTCATT 174

QY 721 AAAGAAGAAACTTAAGCACAGTGAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGA 780  
DB 175 AAAGAAGAAACTTAAGCACAGTGAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGA 234

QY 781 TCTCTGCTGCTGGACAGACTAGCAAGTAATGTCCGCAACCTAGAGAGCTCTATGCTCAG 840  
DB 235 TCTCTGCTGCTGGACAGACTAGCAAGTAATGTCCGCAACCTAGAGAGCTCTATGCTCAG 294

QY 841 AAATTTCTTGGGACCAAGGGCCCTGTCGACAGCCCTACGACAGTGCACAGTACGAGAAG 900  
DB 295 AAATTTCTTGGGACCAAGGGCCCTGTCGACAGCCCTACGACAGTGCACAGTACGAGAAG 354

QY 901 GAGAAGAAATGATGAAGTCCACCGTGTGATGGACCAAGCCATCAACAGCCCATCAACTAC 960  
DB 355 GAGAAGAAATGATGAAGTCCACCGTGTGATGGACCAAGCCATCAACAGCCCATCAACTAC 414

QY 961 CTGGGGGGCGAGTCCCTGCGCCGCTGGTGGCAGAGCCCGGGGGCTTCCGAGGTGGTC 1020  
DB 415 CTGGGGGGCGAGTCCCTGCGCCGCTGGTGGCAGAGCCCGGGGGCTTCCGAGGTGGTC 474

QY 1021 CCGGTTCATCAGCCCGATGTACCAGCTGCACAGGCGCTCGGAGGGCACCCCGGCTCCAC 1080  
DB 475 CCGGTTCATCAGCCCGATGTACCAGCTGCACAGGCGCTCGGAGGGCACCCCGGCTCCAC 534

QY 421 GGAGAACGGCCCTTCCAGTGCATTCAGTGGCGGCTCATTCACCCAGAGGGCAACCTG 480  
DB 421 GGAGAACGGCCCTTCCAGTGCATTCAGTGGCGGCTCATTCACCCAGAGGGCAACCTG 480

QY 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 540  
DB 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTAC 540

QY 541 GCCTGCCCGCGAGGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600  
DB 541 GCCTGCCCGCGAGGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600

QY 601 CACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGAGCTCTTTAGAGGAACATAAA 660  
DB 601 CACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGAGCTCTTTAGAGGAACATAAA 660

QY 661 GAGCGCTGCCACACTACTTGGAAAGCATGGGCTTCCGGGACACACTTACCCAGTCAAT 720  
DB 661 GAGCGCTGCCACACTACTTGGAAAGCATGGGCTTCCGGGACACACTTACCCAGTCAAT 720

QY 721 AAAGAAGAAACTTAAGCACAGTGAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGA 780  
DB 721 AAAGAAGAAACTTAAGCACAGTGAATGGCAGAAGACCTGTGCAAGATAGGATCAGAGAGA 780

QY 781 TCTCTGCTGCTGGACAGACTAGCAAGTAATGTGCGCAACCTTAAGAGCTCTATGCTCAG 840  
DB 781 TCTCTGCTGCTGGACAGACTAGCAAGTAATGTGCGCAACCTTAAGAGCTCTATGCTCAG 840

QY 841 AAATTTCTTGGGACCAAGGGCCCTGTCGACAGCCCTCAGCA-----CAGTCCACGCTACGAG 897  
DB 841 AAATTTCTTGGGACCAAGGGCCCTGTCGACAGCCCTCAGCA-----CAGTCCACGCTACGAG 900

QY 898 AAGGAGAACGAATGATGAAGTCCACAGTGTGGACCAAGCCATCAACAGCCCATCAAC 957  
DB 901 AAGGAGAACGAATGATGAAGTCCACAGTGTGGACCAAGCCATCAACAGCCCATCAAC 960

QY 958 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACGCCCGCCGGCGGCTTCCGAGGTG 1017  
DB 961 TACTTGGGGCCGAGTCCCTGCGCCGCTGGTGCAGACCTCCACCGGTTGTTCTGAAGTG 1020

QY 1018 GTCCCGCTCATACGCGCGATGTACAGCTGCACAGCGCTCGAGGGGCAACCC-----CGCCG 1074  
DB 1021 GTCCCGCTCATACGCGCGATGTACAGCTGCACAGCGCTCGAGGGGCAACCTCGG 1080

QY 1075 TCCAAACACTCGGCCAGGACAGCGCGTGGAGTACCTGCTGCTCTCTCCAAAGGCCAAG 1134  
DB 1081 TCCAAACACTCGGCCAGGACAGCGCGTGGAGTACCTGCTGCTCTCTCCAAAGGCCAAG 1140

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 QY 1141 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACGAGAGC 1200  
 Db 595 CCCTCGGAGCGGAGCGCTCCCGGAGCAACAGCTGCCAAGACTCCACGGACACGAGAGC 654  
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 Db 775 AACTCGCAGGAGCGGCTCCGCGTGTGTACAGCAGCGGAGGAGCAGATGAAGTGTACAAG 834  
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 QY 1501 GAGTTCTCGTCGACATCAACCGAGGAGGAGCAGCGCTTCCACATGAGCTA 1550  
 Db 955 GAGTTCTCGTCGACATCAACCGAGGAGGAGCAGCGCTTCCACATGAGCTA 1004

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 DEFINITION Sequence 7 from patent US 6172278.  
 ACCESSION ARI25033  
 VERSION ARI25033.1 GI:14110423  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1004)  
 AUTHORS Georgopoulos,K.  
 TITLE Ikaros transgenic cells and mice  
 JOURNAL Patent: US 6172278-A 7 09-JAN-2001;  
 FEATURES Location/Qualifiers  
 source 1..1004

BASE COUNT 235 a 328 c 286 g 155 t  
 ORIGIN

Query Match 56.0%; - Score 868; DB 6; Length 1004;  
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 ACCESSION ARI49599  
 VERSION ARI49599.1 GI:15114190  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 1004)
AUTHORS Georgopoulos,K.
TITLE Ikaros: A T cell pathway regulatory gene
JOURNAL Patent: US 628611-A 8 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..1004
BASE COUNT 235 a 328 c 286 g 155 t
ORIGIN
Query Match 56.0%; Score 868; DB 6; Length 1004;
Best Local Similarity 88.8%; Pred. No. 6.2e-136;
Matches 1004; Conservative 0; Mismatches 0; Indels 126; Gaps 1;

QY 421 GGAGAACGGCCCTTCAGTGCATCAATCAGTGCAGGGGCGCTCATTCACCCAGAGGGCAACTG 480
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Db 355 GAGAACGAATGATGAAGTCCCACTGATGGACCAAGCCATCAACACGCCATCAACTAC 414

QY 961 CTGGGGCGCGAGTCCCTGCGCGCGTGGTGCAGACGCCCGCGGCGGTTCGAGAGTGGTC 1020
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RESULT 15
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DEFINITION I03547.1 GI:198286
VERSION DNA-binding transcription factor; Ikaros; Ikaros DNA binding
KEYWORDS protein; transcription; zinc finger protein; zinc-finger
transcription factor.
SOURCE Mus musculus (library: Lambda ZAP EL4) adult cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1550)
AUTHORS Georgopoulos,K., Moore,D.D. and Derfler,B.
TITLE Ikaros, an early lymphoid-specific transcription factor and a
putative mediator for T cell commitment
JOURNAL Science 258 (5083), 808-812 (1992)
MEDLINE 93068267
FEATURES Location/Qualifiers
source 1..1550
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/gene="Ikaros"
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BASE COUNT 385 a 431 c 423 g 311 t
ORIGIN

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Query Match 52.5%; Score 814.8; DB 10; Length 1550;
Best Local Similarity 85.6%; Pred. No. 4.9e-127;
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Db 194 CATGGGTGAACGGCCCTTCAGTGCATCACTGCGGGCGCTTCCTTACCCAGAGGCA 253

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QY	537	CTAGCGCTCCGCGGAGGAGCGCCCTACTGGCCACTGAGGACGCACTCCGTTGGTAA	AA	596
Db	314	CTATGCTCCGCGGAGGAGCGCCCTACCGGCCACTGAGGACGCACTCCGTTGGTAA	AA	373
QY	597	ACCTCAAATGTGATATTGTGGCCGAAGCTATAAACGCGAAGCTCTTTAGAGAACA	AA	656
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QY	777	GAGATCTCTGCTGTGACAGACTAGCAAGTAATGTGCGCAACCTTAAGAGCTCTATGC	CC	836
Db	551	GAGGTCCCTTGTCTGTGACAGGCTGGCAAGCAATGTGCGCAACGTAGAGCTCTATGC	CC	610
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Db	611	TCGAAAATTTCTTGGACAAAGTGCCTGTGACACATGGCCTATGACAGTGCACACTGA	GA	670
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Db	728	CTACTGGGGCGTGTGTCCTGCGCCATTTGTGTGACAGACCCCCCGGTAGCTCCGAG	GT	787
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Db	788	GGTGCCAGTCATCAGCTCCATGTACCGCTGTGCACAGCCCCCTTCAATGGCCCCC	ACG	847
QY	1074	CTCCAACCCTCGGCCGACGACAGCGCTGGAGTACCTGTGCTCTCCAAGGCCAA	AA	1133
Db	848	GTCCAACCATTCAGCACAGA - - CGCGTGGTAACTTGCTGTGCTGTCCAAGGCCAA	AA	904
QY	1134	GTGGTGCCCTCGGAGCGGAGCGTCCCGGACGACAGTGCACAGCTCCAGGAGAC	AA	1193
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Db	1145	GGTGTAAAGTCGACACTGCCCGTCTCTCTGGATCAGTCACTATACCATCCA	AA	1204
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Db	1205	CATGGCTGCCATGCTGCCATGGCTTCGGGATCCCTTTGGTGTGAACATGTGGTGA	AA	1264
QY	1482	CCACGCCAGGACGGTAGAGTTCTCGTCGACATAACGCGAGGGGACCGCTTCCA	AA	1541
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QY	1542	CATGAGCTAA	AA	1551

Db 1325 CCTGAGCTAA 1334

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Wed Aug 28 10:00:38 2002